

*CONRAD*

1633

**ENTERED**RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/377,675ADATE: 07/05/2000  
TIME: 12:26:05Input Set : A:\28480002.app  
Output Set: N:\CRF3\07052000\I377675A.raw

3 <110> APPLICANT: Olwin, Bradley B.  
4 Rosenthal, Richard S.  
6 <120> TITLE OF INVENTION: CHIMERIC FIBROBLAST GROWTH FACTOR PROTEINS, NUCLEIC  
7 ACID MOLECULES, AND USES THEREOF  
9 <130> FILE REFERENCE: 2848-32  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/377,675A  
12 <141> CURRENT FILING DATE: 1999-08-19  
14 <150> PRIOR APPLICATION NUMBER: 60/097,160  
15 <151> PRIOR FILING DATE: 1998-08-19  
17 <160> NUMBER OF SEQ ID NOS: 27  
19 <170> SOFTWARE: PatentIn Ver. 2.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 556  
23 <212> TYPE: DNA  
24 <213> ORGANISM: chimeric sequence  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (8)..(553)  
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32 Met Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys  
33 1 5 10  
35 tgg aaa aag gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97  
36 Trp Lys Lys Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro  
37 15 20 25 30  
39 gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca 145  
40 Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro  
41 35 40 45  
43 aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc 193  
44 Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro  
45 50 55 60  
47 gac ggc cga gtg gag ggg gtc cgc gag aag agc gac cca cac atc aaa 241  
48 Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys  
49 65 70 75  
51 cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg 289  
52 Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val  
53 80 85 90  
55 tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct 337  
56 Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala  
57 95 100 105 110  
59 tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct 385  
60 Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser  
61 115 120 125  
63 aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg 433  
64 Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val  
65 130 135 140  
67 gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct 481

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RAW SEQUENCE LISTING DATE: 07/05/2000  
 PATENT APPLICATION: US/09/377,675A TIME: 12:26:05

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68 Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro  
 69 145 150 155  
 71 ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag 529  
 72 Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln  
 73 160 165 170  
 75 aaa ctc atc tct gaa gag gat ctg tga 556  
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 77 175 180  
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 81 <211> LENGTH: 182  
 82 <212> TYPE: PRT  
 83 <213> ORGANISM: chimeric sequence  
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 87 1 5 10 15  
 89 Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp  
 90 20 25 30  
 92 Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg  
 93 35 40 45  
 95 Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly  
 96 50 55 60  
 98 Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln  
 99 65 70 75 80  
 101 Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala  
 102 85 90 95  
 104 Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys  
 105 100 105 110  
 107 Cys Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn  
 108 115 120 125  
 110 Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu  
 111 130 135 140  
 113 Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln  
 114 145 150 155 160  
 116 Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu  
 117 165 170 175  
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 120 180  
 123 <210> SEQ ID NO: 3  
 124 <211> LENGTH: 556  
 125 <212> TYPE: DNA  
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 130 <222> LOCATION: (11)..(553)  
 132 <400> SEQUENCE: 3  
 133 ggttgtccat atg ggc cgc aaa aaa cgc cgc cag cgc cgc ccg ccg 49  
 134 Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro  
 135 1 5 10  
 137 cag gaa ttc gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97

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138	Gln	Glu	Phe	Ala	Ala	Ala	Gly	Ser	Ile	Thr	Leu	Pro	Ala	Leu	Pro		
139	15				20				25								
141	gaa	gac	ggg	gtt	tct	ggg	gcc	ttc	cca	cca	ggg	cac	ttc	aaa	gac	cca	145
142	Glu	Asp	Gly	Gly	Ser	Gly	Ala	Phe	Pro	Pro	Gly	His	Phe	Lys	Asp	Pro	
143	30				35				40			45					
145	aaa	cgt	ctg	tac	tgc	aaa	aac	ggg	gtt	ttc	ttc	ctg	cgc	atc	cac	ccc	193
146	Lys	Arg	Leu	Tyr	Cys	Lys	Asn	Gly	Gly	Phe	Phe	Leu	Arg	Ile	His	Pro	
147									55			60					
149	gac	ggc	cga	gtg	gac	ggg	gtc	cgc	gag	aag	agc	gac	cca	cac	atc	aaa	241
150	Asp	Gly	Arg	Val	Asp	Gly	Val	Arg	Glu	Lys	Ser	Asp	Pro	His	Ile	Lys	
151					65				70			75					
153	cta	caa	ctt	caa	gca	gaa	gag	aga	ggg	gtt	gtg	tct	atc	aaa	gga	gtg	289
154	Leu	Gln	Leu	Gln	Ala	Glu	Glu	Gly	Val	Val	Ser	Ile	Lys	Gly	Val		
155					80				85			90					
157	tgt	gca	aac	cgt	tac	ctt	gct	atg	aaa	gaa	gat	gga	aga	tta	cta	gct	337
158	Cys	Ala	Asn	Arg	Tyr	Leu	Ala	Met	Lys	Glu	Asp	Gly	Arg	Leu	Leu	Ala	
159					95				100			105					
161	tct	aaa	tgt	gtt	aca	gac	gag	tgt	ttt	ttt	ttt	gaa	cga	ttg	gag	tct	385
162	Ser	Lys	Cys	Val	Thr	Asp	Glu	Cys	Phe	Phe	Phe	Glu	Arg	Leu	Glu	Ser	
163	110				115				120			125					
165	aat	aac	tac	aat	act	tac	cgg	tca	agg	aaa	tac	acc	agt	tgg	tat	gtg	433
166	Asn	Asn	Tyr	Asn	Thr	Tyr	Arg	Ser	Arg	Lys	Tyr	Thr	Ser	Trp	Tyr	Val	
167					130				135			140					
169	gca	ctg	aaa	cga	act	ggg	cag	tat	aaa	ctt	gga	tcc	aaa	aca	gga	cct	481
170	Ala	Leu	Lys	Arg	Thr	Gly	Gln	Tyr	Lys	Leu	Gly	Ser	Lys	Thr	Gly	Pro	
171					145				150			155					
173	ggg	cag	aaa	gct	ata	ctt	ttt	ctt	cca	atg	tct	gct	aag	agc	gaa	cag	529
174	Gly	Gln	Lys	Ala	Ile	Leu	Phe	Leu	Pro	Met	Ser	Ala	Lys	Ser	Glu	Gln	
175					160				165			170					
177	aaa	ctc	atc	tct	gaa	gag	gat	ctg	tga								556
178	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu									
179					175				180								
182	<210>	SEQ	ID	NO:	4												
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189	1				5				10			15					
191	Ala	Ala	Ala	Gly	Ser	Ile	Thr	Thr	Leu	Pro	Ala	Leu	Pro	Glu	Asp	Gly	
192					20				25			30					
194	Gly	Ser	Gly	Ala	Phe	Pro	Pro	Gly	His	Phe	Lys	Asp	Pro	Lys	Arg	Leu	
195					35				40			45					
197	Tyr	Cys	Lys	Asn	Gly	Gly	Phe	Phe	Leu	Arg	Ile	His	Pro	Asp	Gly	Arg	
198					50				55			60					
200	Val	Asp	Gly	Val	Arg	Glu	Lys	Ser	Asp	Pro	His	Ile	Lys	Leu	Gln	Leu	
201					65				70			75			80		
203	Gln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser	Ile	Lys	Gly	Val	Cys	Ala	Asn	
204					85				90			95					

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206 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
207          100      105      110
209 Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
210          115      120      125
212 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
213          130      135      140
215 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
216 145      150      155      160
218 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu Ile
219          165      170      175
221 Ser Glu Glu Asp Leu
222          180
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226 <211> LENGTH: 146
227 <212> TYPE: PRT
228 <213> ORGANISM: Bos taurus
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234 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
235          20          25          30
237 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
238          35          40          45
240 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
241          50          55          60
243 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
244 65          70          75          80
246 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Glu
247          85          90          95
249 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
250          100         105         110
252 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
253          115         120         125
255 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
256          130         135         140
258 Lys Ser
259 145
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 146
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 6
268 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
269 1          5          10          15
271 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
272          20          25          30
274 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
275          35          40          45
277 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser

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Input Set : A:\28480002.app  
 Output Set: N:\CRF3\07052000\I377675A.raw

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278      50          55          60
280 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
281   65          70          75          80
283 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
284          85          90          95
286 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
287          100         105         110
289 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
290          115         120         125
292 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
293          130         135         140
295 Lys Ser
296 145
299 <210> SEQ ID NO: 7
300 <211> LENGTH: 140
301 <212> TYPE: PRT
302 <213> ORGANISM: Bos taurus
304 <400> SEQUENCE: 7
305 Phe Asn Leu Pro Leu Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys
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308 Ser Asn Gly Gly Tyr Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp
309          20          25          30
311 Gly Thr Lys Asp Arg Ser Asp Gly His Ile Gln Leu Phe Leu Cys Ala
312          35          40          45
314 Glu Ser Ile Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Phe
315          50          55          60
317 Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asp
318   65          70          75          80
320 Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
321          85          90          95
323 Tyr Ile Ser Lys Lys His Ala Glu Lys His Trp Phe Val Gly Leu Lys
324          100         105         110
326 Lys Asn Gly Arg Ser Lys Leu Glu Pro Arg Thr His Phe Gly Gln Lys
327          115         120         125
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330          130         135         140
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334 <211> LENGTH: 140
335 <212> TYPE: PRT
336 <213> ORGANISM: Homo sapiens
338 <400> SEQUENCE: 8
339 Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys
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342 Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Tyr Asp
343          20          25          30
345 Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
346          35          40          45
348 Glu Ser Tyr Gly Glu Tyr Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
349          50          55          60

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**VERIFICATION SUMMARY** DATE: 07/05/2000  
**PATENT APPLICATION:** US/09/377,675A TIME: 12:26:06

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